

P. Booker

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/787,097

DATE: 07/19/2001

TIME: 12:16:32

Input Set : A:\00530-089002.txt

Output Set: N:\CRF3\07192001\I787097.raw

PS

4 <110> APPLICANT: Duke-Cohan, Jonathan S.  
5 Schlossman, Stuart F.  
7 <120> TITLE OF INVENTION: REGULATION OF IMMUNE RESPONSES BY ATTRACTIN  
9 <130> FILE REFERENCE: 00530-089002  
11 <140> CURRENT APPLICATION NUMBER: US 09/787,097  
12 <141> CURRENT FILING DATE: 2001-03-13  
14 <150> PRIOR APPLICATION NUMBER: PCT/US99/20948  
15 <151> PRIOR FILING DATE: 1999-09-14  
17 <150> PRIOR APPLICATION NUMBER: US 60/100,137  
18 <151> PRIOR FILING DATE: 1998-09-14  
20 <160> NUMBER OF SEQ ID NOS: 25  
22 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 3597  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Homo sapiens  
29 <220> FEATURE:  
30 <221> NAME/KEY: CDS  
31 <222> LOCATION: (1)...(3594)  
33 <400> SEQUENCE: 1  
34 atg gtg gcc gca gcg gcg gca act gag gca agg ctg agg agg agg acg 48  
35 Met Val Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr  
36 1 5 10 15  
38 gcg gcg acg gca gcg ctc gcg ggc agg agc ggc ggg ccg cac tgt gtc 96  
39 Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Cys Val  
40 20 25 30  
42 aac ggc ggt cgc tgc aac cct ggc acc ggc cag tgc gtc tgc ccc gcc 144  
43 Asn Gly Gly Arg Cys Asn Pro Gly Thr Gly Gln Cys Val Cys Pro Ala  
44 35 40 45  
46 ggc tgg gtg ggc gag caa tgc cag cac tgc ggg ggc cgc ttc aga cta 192  
47 Gly Trp Val Gly Glu Gln Cys Gln His Cys Gly Gly Arg Phe Arg Leu  
48 50 55 60  
50 act gga tct tct ggg ttt gtg aca gat gga cct gga aat tat aaa tac 240  
51 Thr Gly Ser Ser Gly Phe Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr  
52 65 70 75 80  
54 aaa acg aag tgc acg tgg ctc att gaa gga cag cca aat aga ata atg 288  
55 Lys Thr Lys Cys Thr Trp Leu Ile Glu Gly Gln Pro Asn Arg Ile Met  
56 85 90 95  
58 aga ctt cgt ttc aat cat ttt gct aca gag tgt agt tgg gac cat tta 336  
59 Arg Leu Arg Phe Asn His Phe Ala Thr Glu Cys Ser Trp Asp His Leu  
60 100 105 110  
62 tat gtt tat gat ggg gac tca att tat gca ccg cta gtt gct gca ttt 384  
63 Tyr Val Tyr Asp Gly Asp Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe  
64 115 120 125  
66 agt ggc ctc att gtt cct gag aga gat ggc aat gag act gtc cct gag 432  
67 Ser Gly Leu Ile Val Pro Glu Arg Asp Gly Asn Glu Thr Val Pro Glu  
68 130 135 140

ENTERED

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70	gtt gtt gcc aca tca ggt tat gcc ttg ctg cat ttt ttt agt gat gct	480
71	Val Val Ala Thr Ser Gly Tyr Ala Leu Leu His Phe Phe Ser Asp Ala	
72	145 150 155 160	
74	gct tat aat ttg act gga ttt aat att act tac agt ttt gat atg tgt	528
75	Ala Tyr Asn Leu Thr Gly Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys	
76	165 170 175	
78	cca aat aac tgc tca ggc cga gga gag tgt aag atc agt aat agc agc	576
79	Pro Asn Asn Cys Ser Gly Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser	
80	180 185 190	
82	gat act gtt gaa tgt gaa tgt tct gaa aac tgg aaa ggt gaa gca tgt	624
83	Asp Thr Val Glu Cys Glu Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys	
84	195 200 205	
86	gac att cct cac tgt aca gac aac tgt ggt ttt cct cat cga ggc atc	672
87	Asp Ile Pro His Cys Thr Asp Asn Cys Gly Phe Pro His Arg Gly Ile	
88	210 215 220	
90	tgc aat tca agt gat gtc aga gga tgc tcc tgc ttc tca gac tgg cag	720
91	Cys Asn Ser Ser Asp Val Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln	
92	225 230 235 240	
94	ggt cct gga tgt tca gtt cct gta cca gct aac cag tca ttt tgg act	768
95	Gly Pro Gly Cys Ser Val Pro Val Pro Ala Asn Gln Ser Phe Trp Thr	
96	245 250 255	
98	cga gag gaa tat tct aac tta aag ctg ccc aga gca tct cat aaa gct	816
99	Arg Glu Glu Tyr Ser Asn Leu Lys Leu Pro Arg Ala Ser His Lys Ala	
100	260 265 270	
102	gtg gtc aat gga aac att atg tgg gtt gtt gga gga tat atg ttc aac	864
103	Val Val Asn Gly Asn Ile Met Trp Val Val Gly Gly Tyr Met Phe Asn	
104	275 280 285	
106	cac tca gat tat aac atg gtt cta gcg tat gac ctt gct tct agg gag	912
107	His Ser Asp Tyr Asn Met Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu	
108	290 295 300	
110	tgg ctt cca cta aac cgt tct gtg aac aat gtg gtt gtt aga tat ggt	960
111	Trp Leu Pro Leu Asn Arg Ser Val Asn Asn Val Val Arg Tyr Gly	
112	305 310 315 320	
114	cat tct ttg gca tta tac aag gat aaa att tac atg tat gga gga aaa	1008
115	His Ser Leu Ala Leu Tyr Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys	
116	325 330 335	
118	att gat tca act ggg aat gtg acc aat gag ttg aga gtt ttt cac att	1056
119	Ile Asp Ser Thr Gly Asn Val Thr Asn Glu Leu Arg Val Phe His Ile	
120	340 345 350	
122	cat aat gag tca tgg gtg ttg ttg acc cct aag gca aag gag cag tat	1104
123	His Asn Glu Ser Trp Val Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr	
124	355 360 365	
126	gca gtg gtt ggg cac tct gca cac att gtt aca ctg aag aat ggc cga	1152
127	Ala Val Val Gly His Ser Ala His Ile Val Thr Leu Lys Asn Gly Arg	
128	370 375 380	
130	gtg gtc atg ctg gtc atc ttt ggt cac tgc cct ctg tat gga tat ata	1200
131	Val Val Met Leu Val Ile Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile	
132	385 390 395 400	
134	agc aat gtg cag gaa tat gat ttg gat aag aac aca tgg agt ata tta	1248

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135	Ser	Asn	Val	Gln	Glu	Tyr	Asp	Leu	Asp	Lys	Asn	Thr	Trp	Ser	Ile	Leu	
136					405					410					415		
138	cac	acc	cag	ggt	gcc	ctt	gtg	caa	ggg	ggt	tac	ggc	cat	agc	agt	gtt	1296
139	His	Thr	Gln	Gly	Ala	Leu	Val	Gln	Gly	Gly	Tyr	Gly	His	Ser	Ser	Val	
140				420					425					430			
142	tac	gac	cat	agg	acc	agg	gcc	cta	tac	gtt	cat	ggt	ggc	tac	aag	gct	1344
143	Tyr	Asp	His	Arg	Thr	Arg	Ala	Leu	Tyr	Val	His	Gly	Gly	Tyr	Lys	Ala	
144			435					440						445			
146	ttc	agt	gcc	aat	aag	tac	cgg	ctt	gca	gat	gat	ctc	tac	cga	tat	gat	1392
147	Phe	Ser	Ala	Asn	Lys	Tyr	Arg	Leu	Ala	Asp	Asp	Leu	Tyr	Arg	Tyr	Asp	
148		450					455					460					
150	gtg	gat	acc	cag	atg	tgg	acc	att	ctt	aag	gac	agc	cga	ttt	ttc	cgt	1440
151	Val	Asp	Thr	Gln	Met	Trp	Thr	Ile	Leu	Lys	Asp	Ser	Arg	Phe	Phe	Arg	
152	465					470				475						480	
154	tac	ttg	cac	aca	gct	gtg	ata	gtg	agt	gga	acc	atg	ctg	gtg	ttt	ggg	1488
155	Tyr	Leu	His	Thr	Ala	Val	Ile	Val	Ser	Gly	Thr	Met	Leu	Val	Phe	Gly	
156				485					490					495			
158	gga	aac	aca	cac	aat	gac	aca	tct	atg	agc	cat	ggc	gcc	aaa	tgc	ttc	1536
159	Gly	Asn	Thr	His	Asn	Asp	Thr	Ser	Met	Ser	His	Gly	Ala	Lys	Cys	Phe	
160			500						505					510			
162	tct	tca	gat	ttc	atg	gcc	tat	gac	att	gcc	tgt	gac	cgc	tgg	tca	gtg	1584
163	Ser	Ser	Asp	Phe	Met	Ala	Tyr	Asp	Ile	Ala	Cys	Asp	Arg	Trp	Ser	Val	
164			515					520					525				
166	ctt	ccc	aga	cct	gat	tcc	acc	atg	atg	tca	aca	gat	ttg	gcc	att	cca	1632
167	Leu	Pro	Arg	Pro	Asp	Ser	Thr	Met	Met	Ser	Thr	Asp	Leu	Ala	Ile	Pro	
168		530						535				540					
170	gca	gtc	tta	cac	aac	agc	acc	atg	tat	gtg	ttc	ggt	ggt	ttc	aat	agt	1680
171	Ala	Val	Leu	His	Asn	Ser	Thr	Met	Tyr	Val	Phe	Gly	Gly	Phe	Asn	Ser	
172	545					550					555				560		
174	ctc	ctc	ctc	agc	gac	atc	ctg	gta	ttc	acc	tcg	gaa	cag	tgt	gat	gcg	1728
175	Leu	Leu	Leu	Ser	Asp	Ile	Leu	Val	Phe	Thr	Ser	Glu	Gln	Cys	Asp	Ala	
176				565					570					575			
178	cat	cgg	agt	gaa	gcc	gct	tgt	tta	gca	gca	gga	cct	ggt	att	cgg	tgt	1776
179	His	Arg	Ser	Glu	Ala	Ala	Cys	Leu	Ala	Ala	Gly	Pro	Gly	Ile	Arg	Cys	
180			580						585					590			
182	gtg	tgg	aac	aca	ggg	tcg	tct	cag	tgt	atc	tcg	tgg	gcg	ctg	gca	act	1824
183	Val	Trp	Asn	Thr	Gly	Ser	Ser	Gln	Cys	Ile	Ser	Trp	Ala	Leu	Ala	Thr	
184		595						600					605				
186	gat	gaa	caa	gaa	gaa	aag	tta	aaa	tca	gaa	tgt	ttt	tcc	aaa	aga	act	1872
187	Asp	Glu	Gln	Glu	Glu	Lys	Leu	Lys	Ser	Glu	Cys	Phe	Ser	Lys	Arg	Thr	
188		610					615					620					
190	ctt	gac	cat	gac	aga	tgt	gac	cag	cac	aca	gat	tgt	tac	agc	tgc	aca	1920
191	Leu	Asp	His	Asp	Arg	Cys	Asp	Gln	His	Thr	Asp	Cys	Tyr	Ser	Cys	Thr	
192	625					630					635				640		
194	gcc	aac	acc	aat	gac	tgc	cac	tgg	tgc	aat	gac	cat	tgt	gtc	ccc	agg	1968
195	Ala	Asn	Thr	Asn	Asp	Cys	His	Trp	Cys	Asn	Asp	His	Cys	Val	Pro	Arg	
196				645					650					655			
198	aac	cac	agc	tgc	tca	gaa	ggc	cag	atc	tcc	att	ttt	agg	tat	gag	aat	2016
199	Asn	His	Ser	Cys	Ser	Glu	Gly	Gln	Ile	Ser	Ile	Phe	Arg	Tyr	Glu	Asn	

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200		660		665		670	
202	tgc ccc aag gat aac cct atg tac tac tgt aac aag aag acc agc tgc						2064
203	Cys Pro Lys Asp Asn Pro Met Tyr Tyr Cys Asn Lys Lys Thr Ser Cys						
204		675		680		685	
206	agg agc tgt gcc ctg gac cag aac tgc cag tgg gag ccc cgg aat cag						2112
207	Arg Ser Cys Ala Leu Asp Gln Asn Cys Gln Trp Glu Pro Arg Asn Gln						
208		690		695		700	
210	gag tgc att gcc ctg ccc gaa aat atc tgt ggc att ggc tgg cat ttg						2160
211	Glu Cys Ile Ala Leu Pro Glu Asn Ile Cys Gly Ile Gly Trp His Leu						
212	705		710		715		720
214	gtt gga aac tca tgt ttg aaa att act act gcc aag gag aat tat gac						2208
215	Val Gly Asn Ser Cys Leu Lys Ile Thr Thr Ala Lys Glu Asn Tyr Asp						
216		725		730		735	
218	aat gct aaa ttg ttc tgt agg aac cac aat gcc ctt ttg gct tct ctt						2256
219	Asn Ala Lys Leu Phe Cys Arg Asn His Asn Ala Leu Leu Ala Ser Leu						
220		740		745		750	
222	aca acc cag aag aag gta gaa ttt gtc ctt aag cag ctg cga ata atg						2304
223	Thr Thr Gln Lys Lys Val Glu Phe Val Leu Lys Gln Leu Arg Ile Met						
224		755		760		765	
226	cag tca tct cag agc atg tcc aag ctc acc tta acc cca tgg gtc ggc						2352
227	Gln Ser Ser Gln Ser Met Ser Lys Leu Thr Leu Thr Pro Trp Val Gly						
228		770		775		780	
230	ctt cgg aag atc aat gtg tcc tac tgg tgc tgg gaa gat atg tcc cca						2400
231	Leu Arg Lys Ile Asn Val Ser Tyr Trp Cys Trp Glu Asp Met Ser Pro						
232		785		790		795	800
234	ttt aca aat agt tta cta cag tgg atg ccg tct gag ccc agt gat gct						2448
235	Phe Thr Asn Ser Leu Leu Gln Trp Met Pro Ser Glu Pro Ser Asp Ala						
236		805		810		815	
238	gga ttc tgt gga att tta tca gaa ccc agt act cgg gga ctg aag gct						2496
239	Gly Phe Cys Gly Ile Leu Ser Glu Pro Ser Thr Arg Gly Leu Lys Ala						
240		820		825		830	
242	gca acc tgc atc aac cca ctc aat ggt agt gtc tgt gaa agg cct gca						2544
243	Ala Thr Cys Ile Asn Pro Leu Asn Gly Ser Val Cys Glu Arg Pro Ala						
244		835		840		845	
246	aac cac agt gct aag cag tgc cgg aca cca tgt gcc ttg agg aca gca						2592
247	Asn His Ser Ala Lys Gln Cys Arg Thr Pro Cys Ala Leu Arg Thr Ala						
248		850		855		860	
250	tgt gga gat tgc acc agc ggc agc tct gag tgc atg tgg tgc agc aac						2640
251	Cys Gly Asp Cys Thr Ser Gly Ser Ser Glu Cys Met Trp Cys Ser Asn						
252		865		870		875	880
254	atg aag cag tgt gtg gac tcc aat gcc tat gtg gcc tcc ttc cct ttt						2688
255	Met Lys Gln Cys Val Asp Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe						
256		885		890		895	
258	ggc cag tgt atg gaa tgg tat acg atg agc acc tgc ccc cct gaa aat						2736
259	Gly Gln Cys Met Glu Trp Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn						
260		900		905		910	
262	tgt tca ggc tac tgt acc tgt agt cat tgc ttg gag caa cca ggc tgt						2784
263	Cys Ser Gly Tyr Cys Thr Cys Ser His Cys Leu Glu Gln Pro Gly Cys						
264		915		920		925	

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266	ggc tgg tgt act gat ccc agc aat act ggc aaa ggg aaa tgc ata gag	2832
267	Gly Trp Cys Thr Asp Pro Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu	
268	930 935 940	
270	ggt tcc tat aaa gga cca gtg aag atg cct tcg caa gcc cct aca gga	2880
271	Gly Ser Tyr Lys Gly Pro Val Lys Met Pro Ser Gln Ala Pro Thr Gly	
272	945 950 955 960	
274	aat ttc tat cca cag ccc ctg ctc aat tcc agc atg tgt cta gag gac	2928
275	Asn Phe Tyr Pro Gln Pro Leu Leu Asn Ser Ser Met Cys Leu Glu Asp	
276	965 970 975	
278	agc aga tac aac tgg tct ttc att cac tgt cca gct tgc caa tgc aac	2976
279	Ser Arg Tyr Asn Trp Ser Phe Ile His Cys Pro Ala Cys Gln Cys Asn	
280	980 985 990	
282	ggc cac agt aaa tgc atc aat cag agc atc tgt gag aag tgt gag aac	3024
283	Gly His Ser Lys Cys Ile Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn	
284	995 1000 1005	
286	ctg acc aca ggc aag cac tgc gag acc tgc ata tct ggc ttc tac ggt	3072
287	Leu Thr Thr Gly Lys His Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly	
288	1010 1015 1020	
290	gat ccc acc aat gga ggg aaa tgt cag cca tgc aag tgc aat ggg cac	3120
291	Asp Pro Thr Asn Gly Gly Lys Cys Gln Pro Cys Lys Cys Asn Gly His	
292	1025 1030 1035 1040	
294	gcg tct ctg tgc aac acc aac acg ggc aag tgc ttc tgc acc acc aag	3168
295	Ala Ser Leu Cys Asn Thr Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys	
296	1045 1050 1055	
298	ggc gtc aag ggg gac gag tgc cag cta tgt gag gta gaa aat cga tac	3216
299	Gly Val Lys Gly Asp Glu Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr	
300	1060 1065 1070	
302	caa gga aac cct ctc aga gga aca tgt tat tat act ctt ctt att gac	3264
303	Gln Gly Asn Pro Leu Arg Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp	
304	1075 1080 1085	
306	tat cag ttc acc ttt agt cta tcc cag gaa gat gat cgc tat tac aca	3312
307	Tyr Gln Phe Thr Phe Ser Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr	
308	1090 1095 1100	
310	gct atc aat ttt gtg gct act cct gac gaa caa aac agg gat ttg gac	3360
311	Ala Ile Asn Phe Val Ala Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp	
312	1105 1110 1115 1120	
314	atg ttc atc aat gcc tcc aag aat ttc aac ctc aac atc acc tgg gct	3408
315	Met Phe Ile Asn Ala Ser Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala	
316	1125 1130 1135	
318	gcc agt ttc tca gct gga acc cag gct gga gaa gag atg cct gtt gtt	3456
319	Ala Ser Phe Ser Ala Gly Thr Gln Ala Gly Glu Glu Met Pro Val Val	
320	1140 1145 1150	
322	tca aaa acc aac att aag gag tac aaa gat agt ttc tct aat gag aag	3504
323	Ser Lys Thr Asn Ile Lys Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys	
324	1155 1160 1165	
326	ttt gat ttt cgc aac cac cca aat atc act ttc ttt gtt tat gtc agt	3552
327	Phe Asp Phe Arg Asn His Pro Asn Ile Thr Phe Val Tyr Val Ser	
328	1170 1175 1180	
330	aat ttc acc tgg ccc atc aaa att cag gtg caa act gaa caa	3594

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:2226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:2254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:2276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24